

## Refine Search

### Search Results -

Terms	Documents
"Esikova, Irina"[IN]	3

Database:

US Pre-Grant Publication Full-Text Database  
 US Patents Full-Text Database  
 US OCR Full-Text Database  
 EPO Abstracts Database  
 JPO Abstracts Database  
 Derwent World Patents Index  
 IBM Technical Disclosure Bulletins

Search:

L9





### Search History

DATE: Wednesday, September 13, 2006   
 [Purge Queries](#)   
 [Printable Copy](#)   
 [Create Case](#)

<u>Set</u> <u>Name</u>	<u>Query</u>	<u>Hit</u> <u>Count</u>	<u>Set</u> <u>Name</u> result set
side by side			
<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=OR</i>			
<u>L9</u>	"Esikova, Irina"[IN]	3	<u>L9</u>
<u>L8</u>	"Fordham, Dennis"[IN]	2	<u>L8</u>
<u>L7</u>	"Babuka, Susan"[IN]	7	<u>L7</u>
<u>L6</u>	"Shirley, Bret"[IN]	24	<u>L6</u>
<u>L5</u>	"Wolfe, Sidney"[IN]	13	<u>L5</u>
<u>L4</u>	L1 same (guanidine and (ethanol or propanol or alcohol) same (filtration or dialy\$6))	18	<u>L4</u>
<u>L3</u>	L1 same guanidine and (ethanol or propanol or alcohol) same (filtration or dialy\$6)	40	<u>L3</u>
<u>L2</u>	L1 and guanidine and (ethanol or propanol or alcohol) and (filtration or dialy\$6)	6439	<u>L2</u>
<u>L1</u>	(interferon or IFN or INF)	87511	<u>L1</u>

FILE 'MEDLINE, BIOSIS, EMBASE, SCISEARCH, CAPLUS, USPATFULL, PCTFULL'  
ENTERED AT 19:06:14 ON 13 SEP 2006

L1 663358 S (INTERFERON OR IFN OR INF)  
L2 1495 S L1(P) (GUANIDINE) (P) (ETHANOL OR PROPANOL OR ALCOHOL) (P) (DIALY?  
L3 1492 DUP REM L2 (3 DUPLICATES REMOVED)  
L4 645 S L3 AND PY<2001  
L5 7 S L1(S) (GUANIDINE) (S) (ETHANOL OR PROPANOL OR ALCOHOL) (S) (DIALY?  
L6 45 S L1(S) (GUANIDINE) (S) (DIALY? OR FILTRATION)  
L7 3 S WOLFE, SIDNEY/IN  
L8 6 S SHIRLEY, BRET/IN  
L9 10 S BABUKA, SUSAN/IN  
L10 4 S FORDHAM, DENNIS/IN  
L11 7 S ESIKOVA, IRINA/IN

=>

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 08:20:47 ; Search time 71.5 Seconds  
(without alignments)  
1061.509 Million cell updates/sec

Title: US-10-750-076-1  
Perfect score: 874  
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRN 166

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: August 30, 2006, 08:23:37 ; Search time 17 Seconds  
(without alignments)  
854.711 Million cell updates/sec

Title: US-10-750-076-1  
Perfect score: 874  
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRLN 166

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

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OM protein - protein search, using sw model

Run on: August 30, 2006, 08:23:55 ; Search time 48 Seconds  
(without alignments)  
1601.951 Million cell updates/sec

Title: US-10-750-076-1  
Perfect score: 874  
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRN 166

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

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OM protein - protein search, using sw model

Run on: August 30, 2006, 08:24:33 ; Search time 10 Seconds  
(without alignments)  
1143.291 Million cell updates/sec

Title: US-10-750-076-1  
Perfect score: 874  
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRN 166

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 250042 seqs, 68872936 residues

Total number of hits satisfying chosen parameters: 250042

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_New:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

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OM protein - protein search, using sw model

Run on: August 30, 2006, 08:22:55 ; Search time 13 Seconds  
(without alignments)  
1228.614 Million cell updates/sec

Title: US-10-750-076-1  
Perfect score: 874  
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRLN 166

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

OM protein - protein search, using sw model

Run on: August 30, 2006, 08:22:06 ; Search time 90 Seconds  
(without alignments)  
1706.140 Million cell updates/sec

Title: US-10-750-076-1  
Perfect score: 874  
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRLN 166

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 08:20:47 ; Search time 71.5 Seconds  
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1061.509 Million cell updates/sec

Title: US-10-750-076-2  
Perfect score: 869  
Sequence: 1 MSYNLLGFLQRSSNFQSQKL.....RVEILRNFYFINRLTGYLRN 166

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

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3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

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4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
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1143.291 Million cell

updates/sec

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4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
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6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
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2: uniprot\_trembl:\*

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